Review Article – Agriculture

Biotechnological advances for climate change adaptation and mitigation in the case of goat production – A review

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Abstract

Climate change influences goat production directly and indirectly thru its effect on reducing the quality and quantity of feed resources, and increasing spatial and temporal distribution of infectious diseases. The advances of biotechnology now a day's opened an avenue to improve the nutritive value and digestibility of fibrous feeds by using biological methods (e.g., white rot fungi) and through recombinant DNA engineering techniques. Moreover, supplementation of probiotics, enzymes, antibiotics and organic acids modulate the activities and composition of the rumen microbial ecosystem thereby reduce lactic acid content, improve nutrient digestibility, reduce methanogenesis, optimize voluntary fatty acid profiles, and decrease ruminal ammonia production and protein degradation. All these effects increase productive performances and reduce methane emission from goat production. Genetic engineering and introgression of genes between adapted and non-adapted populations have been used to improve the diseases resistance of goat. Vaccines are used to control infectious diseases, increase productivity by modulating hormones or the immune system functions. Immuno-castration and ectoparasite control are also important biotechnological tools. Immunological and molecular techniques diagnostic technologies (PCR, RT-PCR, microarray, proteomic technique, biosensors, fluorescent-in-situ-hybridisation (FISH) and nanotechnologies) are used to detect and identify diseases and their causal agents. However, the aforementioned biotechnological tools are not yet well developed in developing countries like Ethiopia. Therefore, review, evaluation, and implementation of biotechnological tools in goat production in developing countries is paramount to increase production and productivity, and realize the potential use of biotechnology for climate change adaptation and mitigation.

Keywords: Biotechnology; climate change; diseases; animal feed; goat production

Introduction

The domestic goat is one of the most important livestock species most adaptable and geographically widespread, ranging from the mountains of Siberia to the deserts and tropics of Africa (Pereira and Amorim, 2010). There are about 1 billion goats in the world (FAOSTAT, 2016). Goats play imperative roles for rural communities by improving the livelihood of resource-poor farmers by creating alternative employment opportunities, increasing family income from the sale of live animals, skin, and manure. In addition to their contribution to human nutrition in the form of milk and meat, goats also act as an income buffer to the risks associated with erratic climatic changes (Gowane *et al.,* 2017; Gwaze *et al.,* 2009).

Despite their higher economic contribution, small ruminants are susceptible to climate change as they are reared by the poor, unprivileged landless and marginal farmers under extensive system of production. Livestock are not only suffering from climate change but also contribute to climate change through the release of greenhouse gases (GHG). The impact of climate change thus has a twofold implication for the livestock industry, and thereby food security (Scholtz *et al.,* 2013). In addition, climate change impacts animal genetic resources thru catastrophic events, disease epidemics, productivity losses, physiological stress, water availability, agro-ecological changes (fodder quality and quality, host-pathogen interactions) and feed resource availability (Hoffmann, 2010).

The major challenge in animal breeding is maintaining and increasing the productivity of animals under such a variable climatic conditions which reduce quality and availability of feed and induces frequent diseases outbreak. In many developing countries the existing animal breeding practices rely on scoring animals based on their observed physical characteristics or phenotype to determine their breeding value. These conventional methods of selection have limitations of improving for environmental adaptation like climate change. Recently, the emergence of modern biotechnological tools have shown an indispensable promise for climate change adaptation and mitigation through improving intake, digestibility and nutritive value of low-quality forage and improving health and welfare of animals. Moreover, biotechnology is applied to enhance genetic progress through increasing genetic variation (marker-assisted introgression), MAS, reduce generation interval by using assisted reproductive technologies, increase the accuracy of selection and increase the selection intensity. Hence, the use of advanced modern biotechnology tools will help to address the problems associated with climate change and thus help to improve the productivity of goat and reduce GHG emission in a way that alleviates poverty and improves food security. Thus, the aim of this paper is to review biotechnological advances for climate change adaptation and

mitigation in case of goat.

The contribution of goat for climate change and impact of climate change on goat

The world's goat population growth demonstrates a radical change within 55 years (1961 to 2016) (Figure 1). This increase has been taken as an indicator of climate change that goats are becoming prevalent in areas that they were not before and are increasing in number (Kefyalew and Addis, 2016). To this point, livestock are blamed for their contribution to climate change directly and/or indirectly. About 44% of the emissions generated by livestock are CH_4 released during enteric fermentation (eructation in ruminants) and manure decomposition. The rest 27% are in the form of CO_2 emitted during the production and transport of animal products and feed, and 29% are N_2O attributable to manure and fertilizer (Gerber *et al.,* 2013).
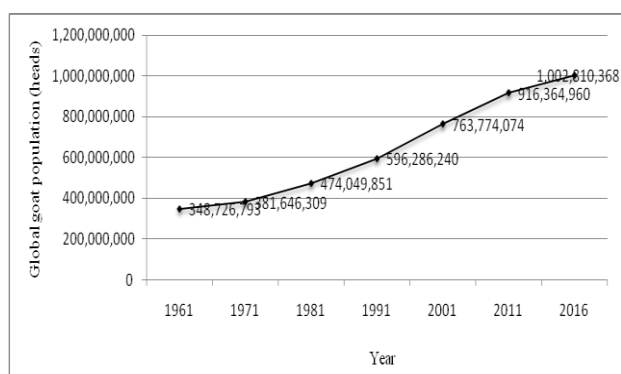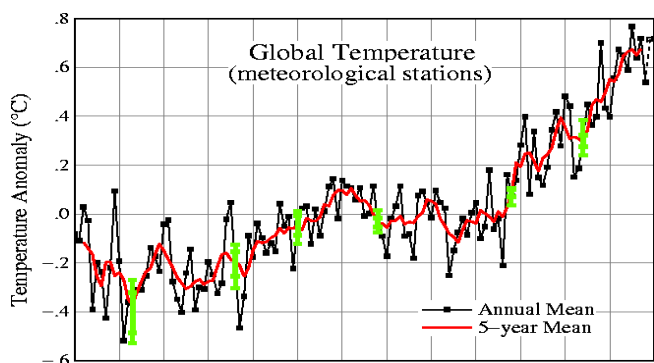

Figure 1. Global goat population growth trend (Source: (FAOSTAT, 2016)

The direct effect of climate change on animal is heat stress. High ambient temperature increases the effort by livestock to dissipate body heat, accordingly resulting in increased body temperature, rate of respiration, heartbeat, and water consumption of animals. The increasing of body temperature is linked with noticeable reduction in feed intake, redistribution in blood flow, and changes in endocrine functions that negatively affect the productive and reproductive performance of livestock (Averós *et al.,* 2008; Hansen, 2004). It is reported that livestock exposed to elevated temperature decreases body weight, growth rate, and body total solids (Marai *et al.,* 2007). The depleted body condition during periods of energy deficiency also reduces heat tolerance (Minka and Ayo, 2009). Figure 2 illustrates an increase in the global temperature anomaly starting from 1970 to 2010.

The induced changes in the agroecosystem like altered feed and nutrient availability as well as disease epidemiology have negative influence on livestock. For many parts of the world, indirect effects of climate change may influence livestock production more pronouncedly than the direct effect (Soumen *et al.,* 2015). Climate significantly influences many infectious diseases especially that are vector-borne. It affects disease-causing pathogens, vectors and hosts and their interactions. Thus, climate change is likely to affect the spatial and temporal distribution and intensity of diseases. For instance, the outbreaks of African horse sickness, bluetongue virus, facial eczema, Rift Valley fever, Peste des Petits Ruminants, and anthrax are triggered by changes in seasonal rainfall profiles and specific weather conditions (Hoffmann, 2010). Similarly, climate change affects the quality and quantity of the forages. Higher temperature increases lignifications and decreases the digestibility of feed resources. The effect of these all, in turn, reduces the productive and reproductive performances of goats.

Table 1. Global GHG emission from goat enteric fermentation and manure management (in gigagram)

Year	Enteric fermentation		Manure management		
	CH_4	CO_2	CH_4	N_2O	CO_2
1961	1743.63	36616.31	55.73	1.31	1577.24
1971	1908.23	40072.86	62.26	1.42	1749.18
1981	2370.25	49775.23	78.24	1.84	2212.19
1991	2981.43	62610.06	99.89	2.38	2834.72
2001	3818.87	80196.28	128.24	3.03	3632.02
2011	4581.82	96218.32	156.03	3.46	4349.46
2016	5014.05	105295.09	171.31	3.71	4747.73

Source: (FAOSTAT, 2016)

Source: NASA-GISS surface temperature analysis (http://climate.nasa.gov/key_indicators#globalTemp).

Figure 2. Global temperature anomaly starting from 1880-2010.

Biotechnology advances as climate change adaptation and mitigation

Genomic tools and transgenic breeding

The use of genomic tools in animal breeding is playing a crucial role in the genetic improvement of productive and adaptive traits of livestock (Elbeltagy, 2017). Using whole genome sequencing, several scholars have reported selection for adaptation traits in tropical livestock species (Kim *et al.,* 2016; Kim *et al.,* 2017; Taye *et al.,* 2017). Now a day, the use of DNA markers such as; SNP assays or genome sequencing is becoming essential for interpreting the genetic basis for adaptation to climatic stress. Recently, Kim *et al.* (2016) analyzed the genome of the hot-arid-adapted Egyptian desert Barki sheep and goats using the data generated from the *ovine* and *caprine* Illumina 50K SNP BeadChips and revealed several candidate genomic regions under selection. The same authors stated that, the genes

under selection are involved in traits for adaptation to hot, arid environments, such as body size and development (*BMP2, BMP4, GJB2 and GJA3*), energy and digestive metabolism (*ALDH1A3, MYH and TRHDE*), thermo-tolerance and melanogenesis (*GNAI3, FGF2 and PLCB1*), and nervous and autoimmune response (*GRIA1, IL1R1, IL2, IL7, IL21*). Most importantly, eight common candidate genes under selection in both *ovine* and *caprine* were also identified, representing shared selection signature of a conserved syntenic segment on sheep chromosome 10 and goat chromosome 12 (Kim *et al.,* 2016). Similarly, Jiang *et al.* (2014) managed to identify genomic signatures associated with interactions between diet, the digestive system, and metabolism in ruminants using genome-sequencing data.

There are clear genetic differences in heat stress tolerance, between tropically adapted breeds experiencing lower body temperatures during heat stress and exotic breeds (non adaptive) (Hansen, 2004; Sahoo *et al.,* 2013). Now a day, it is probably possible to perform genetic selection for resistance to heat stress even for those non adapted breeds. There are specific genes that could be selected which confer increased thermoregulatory ability. It may be possible to identify genes that control cellular resistance to elevated temperature (Sahoo *et al.,* 2013). The superior fertility of tropically adapted breeds during heat stress is a function in large part of the enhanced ability of these breeds to regulate body temperature in response to heat stress. Moreover, certain tropically adapted breeds are more resistant to an elevated temperature at cellular level (Sahoo *et al.,* 2013). Identification of the genes responsible for enhanced cellular resistance to heat shock may allow these genes to be transferred into heat sensitive breeds through conventional or transgenic breeding techniques to produce an animal whose oocytes and embryos have increased resistance to elevated temperature.

Enhancing animal health and welfare

Climate change or variability influences the incidence and prevalence of animal diseases. These links may be spatial, with climate affecting distribution, temporal with weather influencing the timing of diseases outbreak. The diseases transmitted directly between animals in close contact such as; tuberculosis, salmonellosis, FMD, brucellosis, coccidiosis, CCPP, PPR, rabies, rinderpest, and scrapie have associations with climate (Sahoo *et al.,* 2013). In addition to these, anthrax, blackleg, pasteurellosis, leishmaniosis and bluetongue diseases are associated with climate change (Black and Nunn, 2009). Biotechnology play an important role to adopt and mitigate the influences resulted from climate changes through the following techniques.

Increasing disease resistance through genetic engineering

Genetic engineering has the potential to improve disease resistance of animals by introducing specific genes into the genome. Identification of individual genes in the major histocompatibility complex, which influence the immune response, has been instrumental in the recognition of the genetic basis of disease resistance/susceptibility (Lewin, 1989; Wheeler, 2012). It is possible to produce genetically engineer farm animals that are healthier and have superior disease resistance ability through the application of transgenic technology to the desired immune system. For example, the application of nuclear transfer technology (cloning), will enable the amplification of beneficial alleles and the removal of undesirable alleles associated with disease susceptibility via gene knock-out (Lewin, 1989). Moreover, the disease resistant farm animals could easily be produced with embryonic stem cell transgenic approach (Wheeler, 2012).

Increasing disease resistance through genes introgression

The potential use of marker technology in livestock breeding is the transfer of genes that control desired phenotypes between breeds (Wakchaure *et al.,* 2015). If genes controlling resistance to specific disease were identified, it would be possible to transfer them from the resistant indigenous breed into the susceptible improved breed, thus, producing stock that have an increased production potential and resistance to endemic disease (Wakchaure *et al.,* 2015). The introgression of disease resistance genes into the improved breeds could be achieved initially by crossing the indigenous and improved breeds (Wakchaure *et al.,* 2015). The first generation crossbred animals could then be backcrossed to improved breeds and these animals would be genotyped for the genes involved in disease resistance. Subsequently, animals carrying the desired alleles could be selected and backcrossed again to the improved breed. By means of repeated backcrossing and selective breeding from the animals carrying the favorable disease resistance alleles, it is possible to combine the ability of diseases resistance from indigenous breeds and productivity from exotic breeds (Wakchaure *et al.,* 2015).

Vaccines

Vaccines are used to stimulate an animal's immune system to produce the antibodies needed to prevent infection. Recombinant DNA technology has provided the means to produce large quantities of inexpensive vaccines, while a better understanding of the immune system has helped produce vaccines that do a better job of boosting the body's immune system. These engineered products are safer than traditional vaccines (Borroto, 2009). Vaccine produced through biotechnology decreases the risk of reversion to virulence of live vaccines, avoiding contamination with other viruses and reducing damage during storage. Whereas conventional vaccines sometimes revert to virulent (disease-causing) forms the new vaccines can be engineered to eliminate this threat (Babiuk, 2002; Borroto, 2009; Shams, 2005; Vercruysse, 2004). Biotechnology is also producing an entirely new use for vaccines. They are being used to modulate hormones to increase growth rates, improve the efficiency of feed conversion, stimulate milk production, contribute to improved carcass quality and leaner meat, and enhance or suppress reproductive functions (Borroto, 2009). In addition, vaccines made through biotechnology are decreasing the risk of reversion to virulence of live vaccines and of interference with antibodies induced by passive immunization, avoiding contamination with other viruses, reducing damage during storage and other aspects (Shams, 2005; Vercruysse *et al.,* 2004).

Diagnosis technologies

Successful disease control measures require an accurate diagnosis. Advanced diagnostic tests using biotechnological tools enable disease causing agents to be identified, and the impact of disease control programmes to be monitored more

precisely than was previously possible. Molecular epidemiology characterizes pathogens (viruses, bacteria, parasites, and fungi) by nucleotide sequencing, enabling their origins traceable (Fereja, 2016; Madan, 2005). This is particularly important for epidemic diseases, in which pinpointing the source of infection can significantly improve disease control. For example, the molecular analysis of rinderpest viruses has been vital in determining the lineages circulating in the world and instrumental in aiding the Global Rinderpest Eradication Programme (Fereja, 2016; Madan, 2005). Enzyme-linked immunosorbent assays have become the standard means of diagnosing and monitoring many animal diseases worldwide, and PCR technique is especially useful in diagnosing livestock diseases (Fereja, 2016; Madan, 2005). Using DNA testing, carriers can be identified and eliminated from breeding herds. Bulls used for breeding can also be tested to make sure that they are not carriers. DNA test in Japanese Black cattle has identified a gene that leads to anaemia and retarded growth (Madan, 2005).

Real-time polymerase chain reaction (RT-PCR) greatly reduces the problem of cross-contamination, and the ability to electronically process the detected fluorescence in real time obviates the need for subsequent reaction and the electrophoretic run required in traditional PCR (Borroto, 2009). Microarray techniques allow screening for the genotypes of specific parasites and provide major support for epidemiological surveys of veterinary parasites. Proteomic techniques make it possible to identify and characterize the proteins produced by pathogens and are of enormous interest to veterinary diagnosis, enabling the protein expression pattern of viruses, bacteria, and other pathogens to be studied. Proteomics also allows the study of proteins that are expressed or repressed differentially as a result of being attacked by pathogens, which is extremely important for identifying new methods for using vaccines, medicinal products or other means to control pathogens (Borroto, 2009). Other technologies such as biosensors, fluorescent in situ hybridisation (FISH) and nanotechnologies are being incorporated as new veterinary diagnostic tools (Borroto, 2009).

Increasing digestibility of low-quality forages

Climate change and variability which causes an increasing of temperature, modification of rainfall pattern and increasing carbon dioxide levels and can cause harmful effects on both the feed quality and quantity in several ways: through altered herbage growth, decreases herbage quality, variations in pasture composition like grass to legume ratio, with modified concentrations of water-soluble carbohydrates and nitrogen levels per unit dry matter (DM) yields, increased drought occurrences and related DM production losses; and grater precipitation intensity and enhanced nitrogen leaching (Hopkins and Del Prado, 2007). However, it is possible to improve the nutritive value and digestibility of fibrous feed by using chemicals (urea), biological methods (Cone *et al.,* 2012; Yilkal, 2015) and through recombinant DNA engineering techniques.

Biological treatment of crop residues using white rot fungi (WRF) can break the lignocellulose complexes, liberating free cellulose and thus enhancing their feeding value for ruminants. Moreover, it increases the protein and ash contents with a reduction of its fibrous components (NDF, ADF, ADL, cellulose and hemicelluloses) thereby enhance feed intake, digestibility and ultimately animal performance (Mahesh and Mohini, 2013; Yilkal, 2015). Supplementing 2%-6% *Saccharomyces cerevisiae* into low-quality local based-feeds with 16% CP have been found to improve feed intake, weight gain, CP and CF digestibility values of starter local pigs (Ly *et al.,* 2017).

Low-quality forage crops could be genetically modified using recombinant DNA technology with the objective of introducing or enhancing a desirable characteristic in the forage plants. For instance, lignase enzyme produced by the soft-rot fungus (*Phanerochaetechrysosporium*) which causes a high degree of depolymerisation of lignin is used to treat straw. Moreover, the use of recombinant DNA engineering technology could allow the modification of the lignase genes and associate proteins to increase their efficiency and stability and to increases the amount of ligase produced for further treatment of crop residues.

Supplementing with biotechnology product (feed additives)

Organic acids

Organic acids such as malate and fumarate are feed additives that could help to reduce enteric CH_4 emission (Raghavendra *et al.,* 2017). Addition of these organic acids and their sodium salts in the animal diets, causes a shifting of rumen fermentation towards propionate and reduces methane production. For instance; the addition of sodium fumarate has been reported to consistently decrease methane production by 2.3 to 41 % in vitro studies (Ungerfeld *et al.,* 2007), and improved feed digestibility and voluntary fatty acid (VFA) production (Giraldo, 2007). Similarly, malate which is converted to fumarate in the rumen, inhibit methanogenesis and stimulates propionate formation in some in vitro investigations (Tejido, 2005). The possibility of about 60 to 76 % reductions in methane emissions by supplementing fumarate at 100 g/kg to growing lambs was reported by Wood *et al.* (2009). Feeding bromochloromethane (BCM), a halogenated aliphatic hydrocarbon reduced methane production in goat by 33% (21.6 vs. 14.4 L/kg of DMI) compared with non-supplemented animals (Abecia *et al.,* 2012).

Probiotics

Another interesting approach for reducing enteric CH_4 emission is achieved through probiotics supplementation. There are also efforts to shift H_2 from methanogenesis to acetogenesis pathway since the final end product acetate of this pathway can act as additional source of energy for the animals. However, acetogens were found to be less efficient than methanogens in the competition for reducing equivalents in the rumen further, and several attempts to boost their activity were found to be unsuccessful (Raghavendra *et al.,* 2017).

Probiotic supplements also improve intestinal microbial balance (Fuller, 1989). The use of antibiotics as nutritional modifiers could be destroy bacteria, whereas the inclusion of probiotics in feed is designed to encourage certain strains of bacteria in the gut at the expense of less advantageous bacteria (McDonald *et al.,* 2010). Besides, these microorganisms are responsible for the production of vitamins of the B complex and digestive enzymes, and for stimulation of intestinal mucosa immunity, increasing

protection against toxins produced by pathogenic microorganisms. For example, live yeast as probiotic can modulate the activities and composition of the rumen microbial ecosystem, decrease lactic acid content, boost and maintain ruminal pH, improve nutrient digestibility, optimize VFA profiles, and decrease ruminal ammonia production (Wang *et al.,* 2016). Daily supplementations of probiotics (*S. cerevisiae2030)* to dairy goat kids orally at a dosage of 6 ml of 5×10^9 per head improved total weight gain from 3.5kg to 10.12kg (Salvedia and Supungco, 2017). Jinturkar (2009) reported that the mixture of probiotics (mixture of 1g *Lactobacillusacidophillus* +1g *Saccharomyces cerevisiac* per kg feed) was found most effective in reducing the feed requirement, which was only 2.96kg per kg of weight gain than the control (without probiotics) which need 10.0 kg of concentrate per kg weight gain.

Enzymes

In ruminant nutrition, digestive enzymes improve the availability of plant storage polysaccharides (e.g. starch), oils and proteins, which are protected from digestive enzymes by the impermeable cell wall structures. Thus, cellulases can be used to break down cellulose, which is not degraded by endogenous mammalian enzymes. Enzymes are essential for the breakdown of cell-wall carbohydrates to release the sugars necessary for the growth of lactic acid bacteria. Recently, research has shown that supplementation of a wheat by-product diet with cellulose enzyme has increased the digestibility of non-starch polysaccharides from 0.192 to 0.359 and crude protein from 0.65 to 0.71 (McDonald *et al.,* 2010). Amino acid digestibility may also be improved with phytase supplementation. Through supplementation of ZADO® enzyme, total dry matter intake was increased from 76 to 84 g/kg $BW^{0.75}$, digestibility of DM was increased by 11% and average daily gain (ADG) was increased by 6.3 g/kg $BW^{0.75}$ in goat (Salem *et al.,* 2011). According to Zhang and Kornegay (1999), phytase supplementation for finishing pigs increases digestibility of all amino acids, except proline and glycine.

Antibiotics

Antibiotics, antimicrobial pharmaceuticals usually of plant or fungal origin can also be synthesized in the laboratory (Fuller, 1989). Monensin, which is the common ionophore antibiotics is considered as one of the best feed additives which have the properties to reduce enteric methane (CH_4) emission by improving the animal production efficiency (Beauchemin *et al.,* 2008). Monensin is shifting the fermentation pattern towards propionogenesis and thereby causes a reduction of methane (CH_4) emission (McDonald *et al.,* 2010). Monensin enhances the acetate to propionate ratio of the volatile fatty acids in the rumen fluid through enhancing the flow of reducing equivalents to form propionate and also decrease ruminal protozoal numbers. These two mechanisms contribute to the anti-methanogenic effects of monensin and possibly, other ionophores emission (Beauchemin *et al.,* 2008).

Rumen microbial intervention

One of the major indirect impacts of climate change on livestock production is reduction of the digestibility and availability of nutrients from forage feed sources. Cellulose and its bound complexes with other substances are among the components to which ruminal microorganisms are acting

to digest. However, microbes in the rumen have limited capacity to digest cellulose substances as compared to other polysaccharides such as starch or proteins. Therefore, manipulating ruminal microorganisms and the relative population of certain species might help to increase the digestibility of low quality feeds. Manipulation of the rumen system can be achieved either by feed manipulation, host animal manipulation, and/or microbial manipulation (Nagaraja, 2012).

Basically, four groups of microorganisms occupy the rumen: bacteria, methanogens (a methane producing bacterium), protozoa, and fungi. Hence, increasing one and decreasing the other rumen microbes is one method of manipulation. Inclusion of fibrolytic enzymes to animal diet is used to manipulate rumen environment and has been the one most extensively studied in recent years (Kahi and Rewe, 2008; Nagaraja, 2012). Supplementation of the ration with fibrolytic enzymes for goat produced an increase in both the number of rumen bacteria and volatile fatty acids, but not protozoa, counts in rumen fluid. Moreover, it has increased average daily weight gain by 34.7% and efficiency of feed utilization by 28% (Yuangklang *et al.,* 2017).

Another method of manipulating ruminal environment was addition of live microorganisms into the rumen, especially *Aspergillus* and *Saccharomyces* (Gaggìa *et al.,* 2010). The lactate-using bacteria, *Megasphaeraelsdenii*, is commonly found within rumen with very low levels. Dosing of selected *M. elsdenii* strains has proved useful in further reducing the prevalence of acidosis (Meissner *et al.,* 2010). Feeding yeast is used to change ruminal fermentation to reduce methane production, consequently decreasing energy losses during fermentation (Ruiz *et al.,* 2016). A strain of yeast, *Saccharomyces cerevisiae*, which used to stabilize ruminal pH in order to activate fiber-degrading bacteria in the rumen, leading to improved fiber digestibility (Newbold, 1996). Supplementation of fungi is used to enhance ammonia use during fermentation and these effects may enhance bacterial growth and increase microbial protein production (Saxena *et al.,* 2010). Fungi produce cellulolytic and hemicellulolytic enzymes to break down lignin and hemicelluloses, thereby enhance nutrient digestibility of fibrous feeds and increases in VFA concentration and microbial protein production.

Conclusions

Climate change is affecting goat production in many aspects. With this regard, biotechnology is of paramount importance to respond for the influences resulted from climate change thru improving production and reproduction performances, increasing nutrient availability from available feed stuffs, improving immunity and helping for disease diagnostics. However, most of technologies are not yet available in developing countries like Ethiopia. Therefore, introduction and evaluation of those technologies that suite to the conditions of developing countries is important to realize advantages for climate change adaptation and mitigation.

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